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Research Article

Morphological and phylogenetic analyses reveal Xenosporidesmiaceae fam. nov, with seven *Xenosporidesmium* species

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Abstract

This study introduces a new family, Xenosporidesmiaceae, and describes a novel genus, *Xenosporidesmium*, along with a new species, *Xenosporidesmium caohaiense*, based on morphological and phylogenetic analyses. Multi-locus phylogenetic reconstruction (LSU, SSU, ITS, and *rpb*2) revealed that the new family forms a distinct clade, diverging from Sporidesmiales and Distoseptisporales in Sordariomycetes, and supporting its taxonomic independence. The new species, *X. caohaiense*, is characterized by dark brown conidiophores and pale brown, distoseptate conidia with mucilaginous sheaths. Additionally, six previously described *Sporidesmium* species are reclassified into *Xenosporidesmium*. This study emphasizes the significance of molecular data in resolving taxonomic ambiguities among morphologically similar but phylogenetically divergent fungi, thereby contributing to the understanding of freshwater fungal diversity.

Key words: 3 new taxa, asexual morph, phylogeny, Sordariomycetes, taxonomy

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Introduction

Sporidesmium is a common dematiaceous hyphomycetous genus, which is generally recognized as having holoblastic phragmoconidia borne on simple, determinate, or percurrent conidiophores (Ellis 1958; 1971). Since the genus was introduced by Link (1809), numerous taxa have been accommodated to *Sporidesmium*. In a total of 504 epithets of *Sporidesmium* listed in Index Fungorum (August 2025), about 83% of them were proposed before 1992. Based on the diagnostic features such as euseptation/distoseptation, percurrent proliferation, and the absence or presence of conidiophores, Subramanian (1992) reassessed *Sporidesmium* into several genera. Species that have present conidiophores with none or percurrent and irregular proliferations, and euseptate conidia were disposed in *Sporidesmium* sensu stricto. Other genera, such as *Repetophragma* with annellate conidiogenous cells bearing euseptate conidia

on present conidiophores, and *Stanjehughesia* with absent conidiophores and euseptate conidia produced on simple conidiogenous cells, were proposed (Subramanian 1992). Following Subramanian's delimitation, McKenzie (1995) treated thirteen species of sporidesmium-like taxa, including three new species in *Ellisembia* and one in *Sporidesmium*. Hernández-Gutiérrez and Sutton (1997) introduced two genera, *Imimyces* (= *Imicles*) (Shoemaker and Hambleton 2001) based on distoseptate conidia on lageniform, doliiform, or ovoid proliferating conidiogenous cells, and *Linkosia* based on absent conidiophores and solitary and distoseptate conidia on simple conidiogenous cells. Wu and Zhuang (2005) merged *Imicles* into *Ellisembia* and *Penzigomyces* into *Sporidesmium*. The authors also established the genus *Novozymia* based on its annellidically proliferating conidiogenous cells, which differ from those of *Neosporidesmium*.

However, Subramanian's delimitation criteria for *Sporidesmium sensu lato* were rejected by Réblová (1999), who discussed the known connections between sexual morphs and their sporidesmium-like asexual morphs, as well as the morphological differences observed when fungi grow in nature and in culture. For example, *Stanjehughesia larvata* (= *Sporidesmium larvatum*) (Subramanian 1992) produces macronematous conidiophores when growing in nature but has semi-macronematous or micronematous conidiophores when growing in culture (Réblová 1999). Shenoy et al. (2006) revealed that *Sporidesmium* and morphologically similar genera are not monophyletic, being distributed across two distinct fungal classes: Dothideomycetes (e.g., *Sporidesmiella fusiformis*and *Sporidesmium obclavatulum*) and Sordariomycetes (e.g., *Stanjehughesia vermiculata*and *Linkosia fusiformis*). Since then, the polyphyletic nature of sporidesmium-like taxa was demonstrated in many studies (Su et al. 2016; Yang et al. 2018; Liu et al. 2019; Luo et al. 2019).The order Sporidesmiales containing *Sporidesmium sensu stricto* is now placed in Diaporthomycetidae, Sordariomycetes (Crous et al. 2018; Hyde et al. 2020; Dong et al. 2021). Currently, 192 *Sporidesmium* names are listed in Species Fungorum (as of August 2025), with others transferred to more than 50 genera.

During a survey on freshwater fungi in China, two sporidesmium-like taxa were collected and identified on the basis of morpho-phylogenetic evidence. One new family, Xenosporidesmiaceae, is established to accommodate *Xenosporidesmium* gen. nov. and seven species of *Xenosporidesmium*.

Materials and methods

Sampling collection, examination, and isolation

Submerged dead wood samples collected from freshwater in Guizhou Province, China, were placed in zip-lock plastic bags, tagged with the collection information (Rathnayaka et al. 2025), and transported to the laboratory. The samples were then incubated in sterile plastic containers lined with moistened filter paper at room temperature for seven days to promote fungal growth. Motic SMZ 168 Series (Motic, Xiamen, China) and Nikon SMZ-171 (Nikon, Tokyo, Japan) dissecting microscopes were used to observe the fungal colonies and fruiting bodies. Fungal structures were examined and photographed using a Nikon ECLIPSE 80i (Nikon, Tokyo, Japan) compound microscope fitted with a Canon 600D/70D (Canon, Tokyo, Japan) digital camera.

Single-spore isolations were performed according to the method described by Senanayake et al. (2020). Germinated conidia were then aseptically transferred to fresh potato dextrose agar (PDA) plates for further cultivation. Dried specimens were deposited in the Herbarium of Cryptogams, Kunming Institute of Botany, Academia Sinica (HKAS), Kunming, China, and the Herbarium of Guizhou Academy of Agriculture Sciences (GZAAS), Guiyang, China. Pure cultures were deposited at the Guizhou Culture Collection (GZCC), Guiyang, China. The names of the new taxa were registered in Index Fungorum (2025) and Fungal Names (https://nmdc.cn/fungalnames/registe) (Wang et al. 2022).

DNA extraction, PCR amplification, and sequencing

Fresh fungal mycelia grown on potato dextrose agar (PDA) were scraped with a sterilized toothpick and transferred to a 1.5 ml microcentrifuge tube for genomic DNA extraction. Genomic DNA was extracted using the Biospin Fungus Genomic DNA Extraction Kit (BioFlux, China), following the manufacturer's protocol. Four gene regions, LSU, SSU, ITS and *rpb*2 were amplified using the primer pairs LR0R/LR5, NS1/NS4, ITS5/ITS4and *rpb*2-5F/ *rpb*2-7cR, respectively (Liu et al. 1999; Vilgalys and Hester 1990; White et al. 1990). The PCR amplification reactions were performed in a 25 µL reaction volume, comprising 1 µL of DNA, 1 µL of each forward and reverse primer, and 22 µL of 1.1 × T3 Super PCR Mix (Qingke Biotech, Chongqing, China). The conditions for the polymerase chain reaction (PCR) correspond to the reaction conditions reported by Liu et al. (2019). The PCR products were detected by 1% agarose gel electrophoresis, and the sequencing results were provided by Beijing Tsingke Biotechnology Co., Ltd.

Phylogenetic analyses

The sequences incorporated in this study were downloaded from GenBank (Table 1; https://www.ncbi.nlm.nih.gov/). The single gene datasets (LSU, SSU, ITS, and *rpb*2) were aligned using MAFFT v.7.473 (https://mafft.cbrc.jp/alignment/server/, (Katoh and Standley 2013)) and trimmed using trimAl.v1.2rev59 software (Capella-Gutierrez et al. 2009) with the 'gappyout' option. Multiple gene alignments were merged using SequenceMatrix 1.7.8 (Vaidya et al. 2011).

The maximum likelihood (ML) tree was conducted in the IQ Tree webserver (http://iqtree.cibiv.univie.ac.at/) (Nguyen et al. 2014) with 1,000 ultrafast bootstrap (BS) replicates. The substitution model option was set to auto. Maximum likelihood bootstrap supports (ML-BS) equal to or greater than 75% are marked above or below each branch.

Bayesian inferences (BI) were performed using a Markov chain Monte Carlo (MCMC) algorithm in MrBayes 3.2.6 (Ronquist et al. 2012). The best-fit substitution models for each single gene alignment were decided by MrModeltest 2.3 (Nylander 2008) under the Akaike Information Criterion (AIC). Two parallel runs of four simultaneous Markov chains were performed for 10,000,000 generations, or the searches were stopped when the average standard deviation of split frequencies was below 0.01 (stopval = 0.01). Trees were sampled every 1,000th generations. The first 25% of trees were set as burn-in and discarded. The remaining trees were used to calculate posterior probabilities (BYPP). BYPP supports equal to or greater than 0.95 and is marked above or below each branch.

Table 1. Taxa used in this study and their GenBank accession numbers.

Species	Strain	Type	LSU	SSU	ITS	*rpb2*
Acidothrix acidophila	CBS 136259		MH877622	NA	NA	NA
Acrodictys aquatic	MFLUCC 18-0356		MG835712	NA	MG835711	NA
Acrodictys bambusicola	CGMCC 3.18641		KX033564	KX033535	KU999973	NA
Acrodictys chishuiensis	HKAS 112618	T	OP377909	OP377995	OP377810	OP473084
Acrodictys effuse	GZAAS 20-0446	T	OP377936	NA	MW133879	NA
Afroraffaelea ambrosiae	CBS 141678		NG_057115	NG_061251	NA	NA
Amplistroma caroliniana	BEO 9923		FJ532377	NA	NA	NA
Annulatascus velatisporus	MFLUCC 16-1441		KY244031	KY244032	NA	NA
Annulatascus velatisporus	HKUCC 3701	T	AF132320	NA	NA	NA
Annulusmagnus triseptatus	A54 10A		AY590286	NA	NA	NA
Annulusmagnus triseptatus	CBS 128831	T	GQ996540	JQ429242	NA	JQ429258
Aquapteridospora lignicola	MFLUCC 15-0377	T	KU221018	NA	NA	NA
Aquapteridospora linzhiensis	KUNCC 10420	T	OQ970576	NA	OP626343	NA
Aquapteridospora hyaline	GZCC 22-0072	T	ON527945	NA	ON527937	NA
Ascitendus austriacus	CBS 102665		NG_056942	NG_061014	NA	NA
Ascotaiwania latericolla	ICMP 22739		MN699407	NA	NR_173185	MN704312
Atractospora reticulate	CBS 127884		KT991660	NA	NA	KT991649
Aureobasidium pullulans	CBS 584.75		NG_055734	NG_062753	NR_144909	NA
Barbatosphaeria barbirostris	CBS 121149		EF577059	KM492851	NA	KM492903
Barbatosphaeria dryina	CBS 127691		KM492864	KM492852	KM492890	KM492904
Barbatosphaeria neglecta	CBS 127693		KM492868	KM492856	NA	NA
Barretomyces calatheae	CBS 129274		KM484950	NA	KM484831	NA
Brachysporium nigrum	MR 1346		KT991662	KT991643	NA	KT991652
Bullimyces communis	AF281.5		JF775587	JF758619	NA	NA
Bussabanomyces longisporus	CBS 125232		KM484951	NG_061183	KM484832	NA
Calosphaeria pulchella	CBS 115999		AY761075	AY761071	NA	GU180661
Canalisporium caribense	SS03839		GQ390268	GQ390253	GQ390283	NA
Cancellidium atrobrunneum	MFLUCC 20-0100		MT422740	MT422726	NA	NA
Ceratolenta caudate	CBS 125234		JX066704	NG_061136	NA	JX066699
Chaetopsina pinicola	CBS136444		NG_058865	NA	NA	NA
Coniolariella gamsii	CBS 117677		MH874576	NA	NA	NA
Conlarium duplumascospora	CGMCC 3.14938	T	JN936991	JN936987	NR_138382	NA
Cryphonectria parasitica	CMW 7084		JN940858	JN938760	JN942325	NA
Cryptadelphia groenendalensis	SMH 3767		EU528001	NA	NA	NA
Cryptadelphia groenendalensis	SH 12		EU528007	NA	NA	NA
Cytospora thailandica	MFLUCC 17-0263		NG_064536	NA	NA	MH253464
Deightoniella roumeguerei	CBS 128780		JF951176	NA	JF951153	NA
Diaporthe eres	AR3538		AF408350	NA	NA	NA
Dictyosporella aquatic	MD1302		KT241022	KT241023	NA	NA
Distoseptispora aquatic	MFLUCC 15-0374	T	KU376268	NA	MF077552	NA
Distoseptispora fluminicola	DLUCC 0391	T	MG979762	NA	MG979755	NA
Distoseptispora fluminicola	MFLUCC 15-0417	T	KU376270	NA	MF077553	NA
Distoseptispora guttulata	MFLUCC 16-0183	T	MF077554	MF077532	MF077543	NA
Distoseptispora obpyriformis	MFLUCC 17-1694	T	MG979764	NA	NA	MG988415
Distoseptispora rostrata	MFLUCC 16-0969	T	MG979766	NA	MG979758	MG988417
Distoseptispora tectonae	MFLUCC 12-0291	T	KX751713	NA	KX751711	KX751708
Dothidea hippophaeos	CBS 188.58		DQ678048	NA	MH857750	NA
Dothidea insculpta	CBS 189.58		MH869284	DQ247810	NA	NA

Species	Strain	Type	LSU	SSU	ITS	*rpb2*
Flabellascus tenuirostris	CBS 138680		NG_058200	NA	NR_136138	NA
Flabellascus tenuirostris	CBS 138690		KT716458	NA	KT716467	NA
Fluminicola saprophytica	MFLUCC 15-0976		MF374367	MF374375	NA	MF370954
Fragosphaeria purpurea	CBS 133.34		AB189154	AF096176	NA	NA
Gnomoniopsis chamaemori	CBS 803.79		EU255107	NA	NA	NA
Halazoon melhae	MF819		GU252143	GU252144	NA	NA
Harknessia eucalypti	CPC 13643		JQ706215	NA	NA	NA
Hawksworthiomyces taylorii	CMW 20741	T	NG_059701	NA	NR_155176	NA
Hydea pygmea	NBRC33069		GU252133	GU252134	NA	NA
Jattaea prunicola	STEU 6201		EU367456	EU367462		NA
Jennwenomyces navicularis	BCRC FU30872		MT224909	NA	MT224914	NA
Jobellisia fraternal	SMH 2863		AY346285	NA	NA	NA
Jobellisia guangdongensis	HMAS 251240		NG_068733	NA	NR_138381	NA
Jobellisia guangdongensis	DQ09		MN733255	NA	MN733257	NA
Jobellisia luteola	SMH 2753		AY346286	NA	NA	NA
Junewangia sphaerospora	CGMCC 3.18655		KX033572	KX033543	KU999981	NA
Kohlmeyeriopsis medullaris	CBS 117849		KM484968	NA	KM484852	NA
Lanspora coronate	AFTOL-ID 736		U46889	NA	NA	DQ470899
Lulworthia fucicola	ATCC 64288		AY878965	AY879007	NA	NA
Magnaporthe salvinii	M 21		JF414887	JF414862	NA	NA
Myrmecridium iridis	CPC 25084		KR476777	NA	KR476744	NA
Nakataea oryzae	CBS 252.34		MH867001	NA	KM484862	NA
Natarajania thailandica	MFLUCC 18-0394		MT371074	NA	NA	MT364367
Neomyrmecridium guizhouense	GZCC 20-0008		MT002307	NG_068427	NA	MT023016
Neomyrmecridium septatum	CBS 145073		NG_066289	NA	NR_161133	MK047544
Neospadicoides lignicola	MFLUCC 17-2444	T	MK849854	MK828309	MK828702	MN124532
Ophiostoma piliferum	AFTOL-ID 910		DQ470955	DQ471003	NA	DQ470905
Papulosa amerospora	AFTOL-ID 748		DQ470950	DQ470998	NA	DQ470901
Pararamichloridium livistonae	CPC 32156		MG386084	NA	NA	NA
Phaeoacremonium chiangmaiense	CMUB 40065	T	PQ699722	NA	PQ699720	NA
Phaeoacremonium chiangmaiense	CMU511		PQ699723	NA	PQ699721	NA
Phaeoacremonium fraxinopennsylvanica	MR 3064		HQ878595	HQ878600	NA	HQ878609
Phaeoacremonium minimum	CBS 6580		AY761082	AY761068	NA	DQ470913
Phialemoniopsis ocularis	UTHSC 05-2527		HE599266	NA	HE599281	NA
Phomatospora bellaminuta	AFTOL-ID 766		FJ176857	FJ176803	NA	FJ238345
Pleurostoma ootheca	CMU 23858		AY761079	AY761074	NA	HQ878606
Polylobatispora deltoidea	NBRC 106820		LC495605	NA	LC495612	NA
Pseudoproboscispora thailandensis	MFLUCC 15-0989		NG_059843	NG_063646		NA
Pseudostanjehughesia aquitropica	MFLUCC 16-0569		MF077559	MF077537	MF077548	NA
Pyricularia grisea	BR0029		KM484995	NA	KM484880	NA
Pyriculariopsis parasitica	HKUCC5562		DQ341514	NA	NA	NA
Rhamphoria delicatula	CBS 132724		MH878338	NA	NA	NA
Rhodoveronaea varioseptata	CBS 431.88		EU041870	NA	EU041813	NA
Rubellisphaeria abscondita	CBS 132078		KT991666	KT991646	NA	KT991657
Savoryella lignicola	NF00204		HQ446378	HQ446300	NA	NA
Spadicoides bina	CBS 137794		KY931824	KY931881	KY931796	KY931851

Species	Strain	Type	LSU	SSU	ITS	*rpb2*
Sporidesmiella hyalospermum	MFLUCC 18-1312		MK849839	NA	MK828688	MN124520
Sporidesmium appendiculatum	MFLU 18-0981	T	MW287774	NA	NR_172451	NA
Sporidesmium aquaticum	MFLUCC 15-0420		KU376273	NA	NA	NA
Sporidesmium bambusicola	HKUCC 3578		DQ408562	NA	NA	NA
Sporidesmium dalbergiae	CPC 38960		MZ064481	NA	MZ064424	NA
Sporidesmium diplazii	KUNCC 23-13844	T	PQ671194	NA	PQ671275	PQ662531
Sporidesmium dulongense	MFLUCC 17-0116	T	NG_073631	NA	NR_171826	NA
Sporidesmium minigelatinosa	NN47497		DQ408567	NA	NA	DQ435090
Sporidesmium pronephrii	KUNCC 23-13909	T	PQ671195	NA	PQ671276	PQ662532
Sporidesmium pyriformatum	MFLUCC 15-0620		KX710141	NA	KX710146	MF135649
Sporidesmium thailandense	MFLUCC 15-0964		MF374370	NA	MF374361	MF370955
Sporidesmium tratense	MFLUCC 17-2392	T	OP377975	OP378050	OP377889	OP473120
Sporidesmium tropicale	MFLUCC 16-0185	T	MF077562	MF077539	MF077551	MF135646
Sporidesmium tropicale	HKUCC 10838		DQ408560	NA	NA	NA
Striaticonidium cinctum	CBS 932.69	T	KU847265	NA	KU847239	KU847290
Synnemasporella toxicodendri	CFCC 52097		MG682029	NA	MG682089	MG682049
Thailandiomyces bisetulosus	BCC00018		EF622230	EF622229	NA	NA
Thyridium vestitum	AFTOL-ID 172		AY544671	AY544715	NA	DQ470890
Tirisporella beccariana	BCC36738		JQ655451	JQ655453	NA	NA
Togniniella acerosa	ICMP 18256		AY761076	AY761073	NA	GU180660
Volutella consors	CBS 189.73		MH878487	NA	NA	NA
Xenocylindrocladium serpens	CBS 128439		MH876378	NA	NA	NA
Xenosporidesmium aquaticivaginatum	MFLUCC 15-0624		KX710142	MF077541	KX710147	MF135647
Xenosporidesmium aquaticivaginatum	KUNCC 23-13373		OR600972	OR743215	OR589324	OR820910
Xenosporidesmium caohaiense	**GZCC 19-0534**	**T**	**MZ227226**	**MW134698**	**MW133918**	**NA**
Xenosporidesmium caohaiense	**GZCC 19-0533**		**MZ227225**	NA	**MW133917**	**NA**
Xenosporidesmium filiforme	HKAS 130435	T	OR600973	OR743216	OR589325	OR820911
Xenosporidesmium guizhouense	CGMCC 3.19605	T	MK818586	MK818588	MK818587	MK828516
Xenosporidesmium guttulatum	KUNCC 23-13374	T	PP994882	OR743217	OR589326	OR820912
Xenosporidesmium nujiangense	DLUCC 983	T	NG_088244	MZ420748	NR_175741	MZ442695
Xenosporidesmium olivaceoconidium	MFLUCC 15-0380		KX710139	MF077542	KX710144	MF135648
Xylaria hypoxylon	AFTOL-ID 51		AY544648	NA	NA	DQ470878
Xylolentia brunneola	PRA 13611		MG600398	NA	MG600394	MG600402

Note: "T" indicates ex-type strains. Newly generated sequences are inbold. "NA" indicates the unavailable data in GenBank.

Phylogenetic trees were visualized using FigTree v1.4.4 and subsequently edited in Adobe Illustrator CC 2019 (v23.1.0; Adobe Systems, USA). Photo-plate and scale bars were prepared using Adobe Photoshop CC 2019 (Adobe Systems, USA) and the Tarosoft (R) Image Framework program, respectively.

Phylogenetic results

The phylogenetic placement of the two newly obtained strains was determined through multi-locus phylogenetic analysis. The concatenated sequence matrix comprised 3,292 characters (LSU: 1–822, SSU: 823–1,800, ITS: 1,801–2,273, and *rpb2*: 2,274–3,292) across 127 taxa. Both ML and BYPP analyses produced congruent topologies. The best ML tree with a final likelihood value of -60836.732 is presented in Fig. 1.

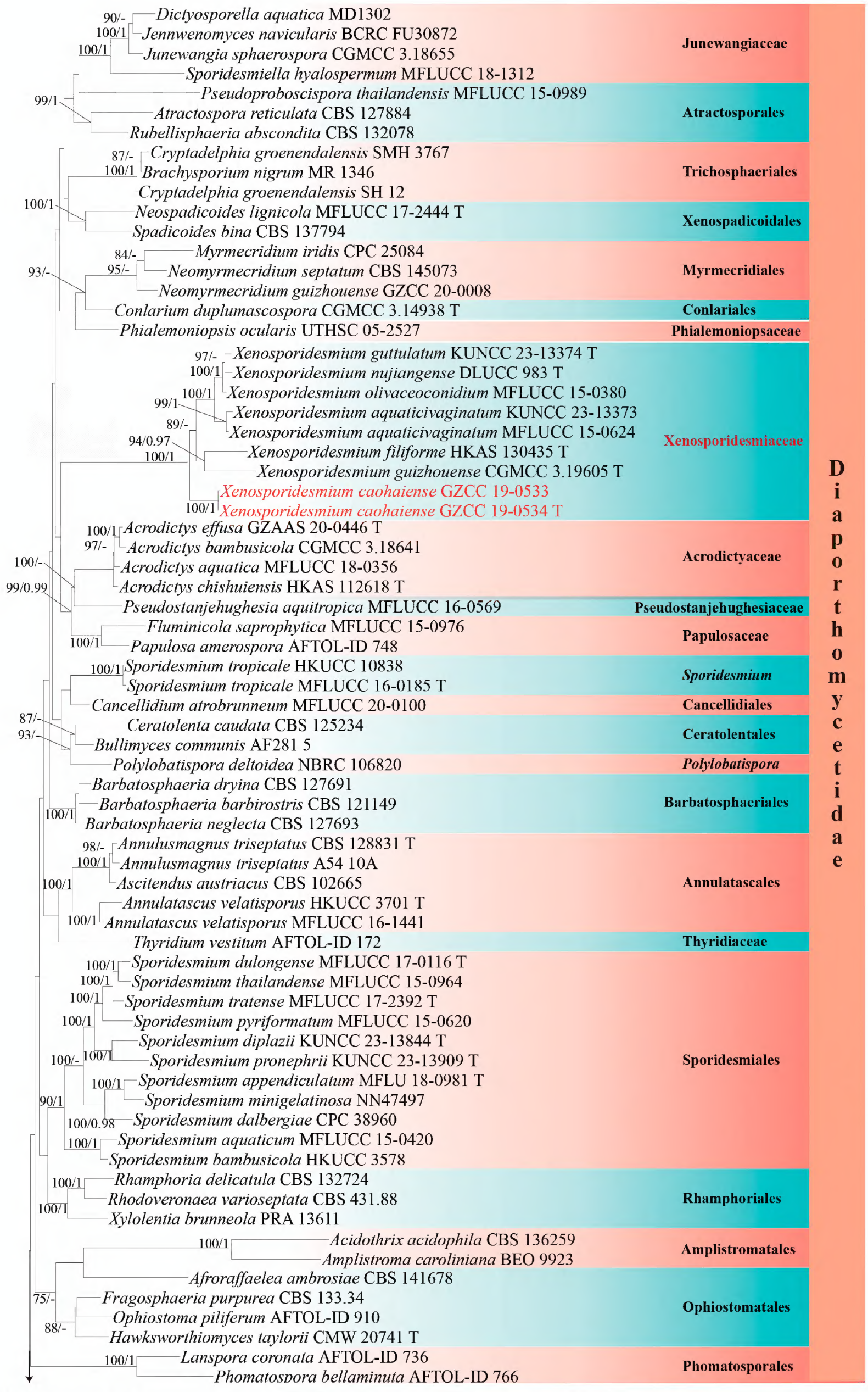

Figure 1. Phylogenetic tree generated from ML analysis based on the combined LSU, SSU, ITS, and *rpb*2 sequence data. Bootstrap support values for ML (≥ 75%) and BYPP (≥ 0.95) are indicated near their respective nodes. The tree is rooted with *Aureobasidium pullulans* CBS 584.75, *Dothidea hippophaeos* CBS 188.58, and *Dothidea insculpta* CBS 189.58. Newly obtained strains are in red.

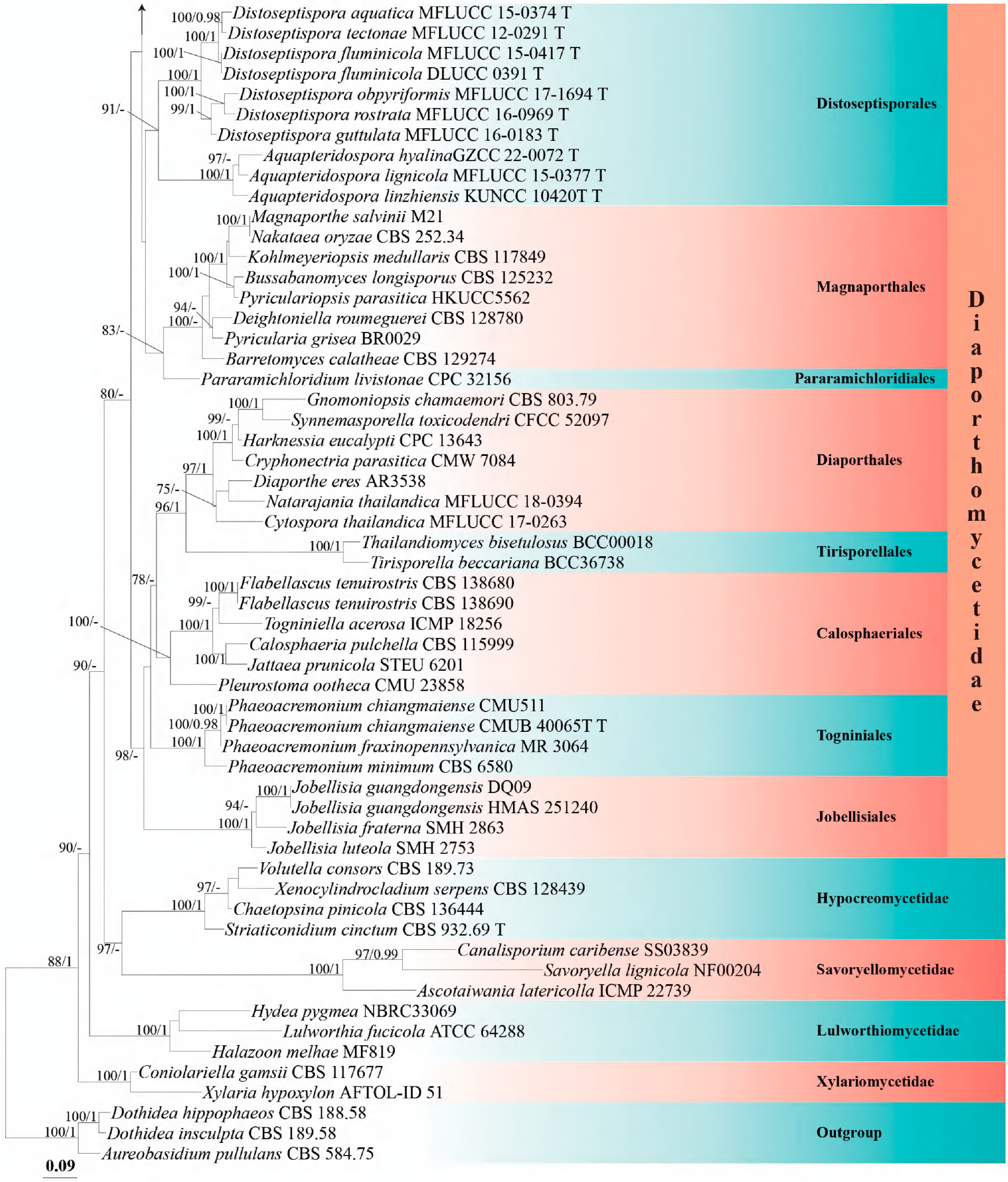

Figure 1. Continued.

Based on the multi-gene phylogenetic analysis (Fig. 1), our isolates (GZCC 19-0533 and GZCC 19-0534) represent a distinct species of *Xenosporidesmium*, forming a well-supported basal clade within the genus. Notably, this new species clusters with six other taxa—*X. aquaticivaginatum*, *X. filiforme*, *X. guizhouense*, *X. guttulatum*, *X. nujiangense*, and *X. olivaceoconidium*—to comprise a monophyletic lineage that is phylogenetically distinct from Sporidesmiales. Furthermore, this clade is phylogenetically sister to three *incertae sedis*

families in Diaporthomycetidae (Acrodictyaceae, Papulosaceae and Pseudostanjehughesiaceae). Given the consistent molecular divergence and morphological uniqueness, we propose recognition of this clade as a new family, Xenosporidiaceae (Diaporthomycetidae, family *incertae sedis*).

Taxonomy

Xenosporidesmiaceae L. L. Liu & Z. Y. Liu, fam. nov.
Fungal Names: FN 572989

Etymology. Referring to the name of the type genus.

Description. ***Colonies*** on nature substrate effuse, hairy, scattered or in small groups. ***Conidiophores*** macronematous, mononematous, solitary, cylindrical, straight or slightly flexuous, dark brown, septate. ***Conidiogenous cells*** holoblastic, monoblastic, integrated, terminal, cylindrical, smooth, pale to dark brown. ***Conidia*** acrogenous, solitary, obclavate, pale brown to olivaceous, paler at the apex, tapering gradually towards the apex, smooth, straight or curved, distoseptate, with a mucilaginous sheath or apical appendage.

Type genus. *Xenosporidesmium* L. L. Liu & Z. Y. Liu, gen. nov.

Notes. The new family Xenosporidesmiaceae is established to accommodate a distinct lineage comprising six *Sporidesmium* species and one new species described herein. This lineage forms a highly supported clade (ML/BS = 100%, BYPP = 1) in the multi-gene phylogeny (LSU, SSU, ITS, and *rpb*2), diverging from both Sporidesmiales and Distoseptisporales. All members share pale brown, sheathed or appendaged conidia and are exclusively associated with freshwater habitats (Hyde et al. 2016; Liu et al. 2019; Wang et al. 2024). The family is proposed to resolve the phylogenetic placement of these morphologically similar yet evolutionarily distinct taxa, and its establishment aims to avoid taxonomic confusion with the currently recognized *Sporidesmium sensu stricto*.

Xenosporidesmium **L. L. Liu & Z. Y. Liu, gen. nov.**
Index Fungorum: IF904245

Etymology. "Xeno-" means different, "*Xenosporidesmium*" reflects that, although this fungus resembles *Sporidesmium* in morphology, it is genetically distinct and phylogenetically separate.

Type species. *Xenosporidesmium aquaticivaginatum* (Jiang Yang & K.D. Hyde) L. L. Liu & Z. Y. Liu, comb. nov.

Description. ***Saprobic*** on dead wood. **Sexual morph**: Undetermined. **Asexual morph**: ***Colonies*** on nature substrate effuse, hairy, scattered or in small groups. ***Conidiophores*** macronematous, mononematous, solitary, cylindrical, straight or slightly flexuous, dark brown, septate. ***Conidiogenous cells*** holoblastic, monoblastic, integrated, terminal, determinate or with one percurrent proliferation, cylindrical, smooth, pale to dark brown. ***Conidia*** acrogenous, solitary, obclavate, pale brown to olivaceous, paler at the apex, tapering gradually towards the apex, smooth, straight or curved, distoseptate, with a mucilaginous sheath or apical appendage.

Notes. The new genus *Xenosporidesmium* is established to accommodate seven species, including one newly discovered taxon and six species previously classified in *Sporidesmium*. *Xenosporidesmium aquaticivaginatum* (=*Sporidesmium aquaticivaginatum*) is designated as the type species because its epithet reflects the aquatic habitat preference characteristic of this genus, although it was published concurrently with *X. olivaceoconidium* in the same work (Hyde et al. 2016). In this study, we introduce one new *Xenosporidesmium* species and transfer *Sporidesmium aquaticivaginatum*, *S. filiforme*, *S. guizhouense*, *S. guttulatum*, *S.nujiangens*, and *S. olivaceoconidium* to *Xenosporidesmium* based on phylogenetic analyses.

Xenosporidesmium caohaiense **L. L. Liu & Z. Y. Liu, sp. nov.**

Index Fungorum: IF904247

Fig. 2

Etymology. The epithet "caohaiense" refers to the type location, Caohai National Nature Reserve.

Holotype. HKAS 150269

Description. ***Saprobic*** on decaying submerged wood in freshwater habitats. **Sexual morph**: Unknown. **Asexual morph**: Hyphomycetous. ***Colonies*** on natural substrate effuse, hairy, dark brown, scattered or in small groups, velvety. ***Mycelium*** mostly immersed, composed of pale to brown, branched, septate, smooth hyphae. ***Conidiophores*** macronematous, mononematous, erect, solitary, straight or slightly flexuous, unbranched, cylindrical, dark brown, 1–3-septate, 25.5–50 × 3.5–6 µm ($\bar{x}$ = 37 × 4.5 µm, n = 20). ***Conidiogenous cells*** monoblastic, integrated, terminal, cylindrical or lageniform, pale brown, (6–)9–14.5 × 2.5–5.5 µm ($\bar{x}$ = 11 × 4 µm, n = 20). ***Conidia*** 35–51 × 7.5–11 µm ($\bar{x}$ = 42 × 9 µm, n = 20), acrogenous, solitary, obclavate, pale brown, straight or slightly flexuous, apically rostrate, hyaline to pale brown, often with a mucilaginous sheath, truncate at the base, 8–13-distoseptate, guttulate, smooth-walled, thin-walled.

Culture characteristics. Conidia germinating on PDA medium within 12 h. Germ tubes produced from the apex. Colonies on PDA medium reaching 20 mm diam. after 3 weeks at 25 °C, circular, flat, centrally umbonate, with velvety, white to pale yellow mycelium on the surface; in reverse pale yellow with entire margin.

Material examined. China • Guizhou Province, Bijie City, Weining District, Caohai National Nature Reserve, on decaying wood submerged in a freshwater lake, 4 October 2018, L.L. Liu, 18C-69 (HKAS 150269, holotype; GZAAS 20-0429, isotype), ex-type cultures GZCC19-0534; China • Guizhou Province, Zunyi City, Chishui District, on decaying wood submerged in a freshwater stream, 16 July 2019, J. Yang, CS2-6-1 (HKAS 150268), living cultures GZCC 19-0533.

Notes. *Xenosporidesmium caohaiense* forms a distinct lineage and clusters within the *Xenosporidesmium* clade by high support (ML-BS = 100%, BYPP = 1) in the phylogenetic tree, indicating a close relationship with other *Xenosporidesmium*. The morphological differences with other *Xenosporidesmium* species are shown in Table 2. *Xenosporidesmium filiforme* is distinguished from other *Xenosporidesmium* species by possessing an apical appendage. *Xenosporidesmium caohaiense* can be differentiated from all other species (except *X. olivaceoconidium*) based on the dimensions of its conidiophores, conidiogenous

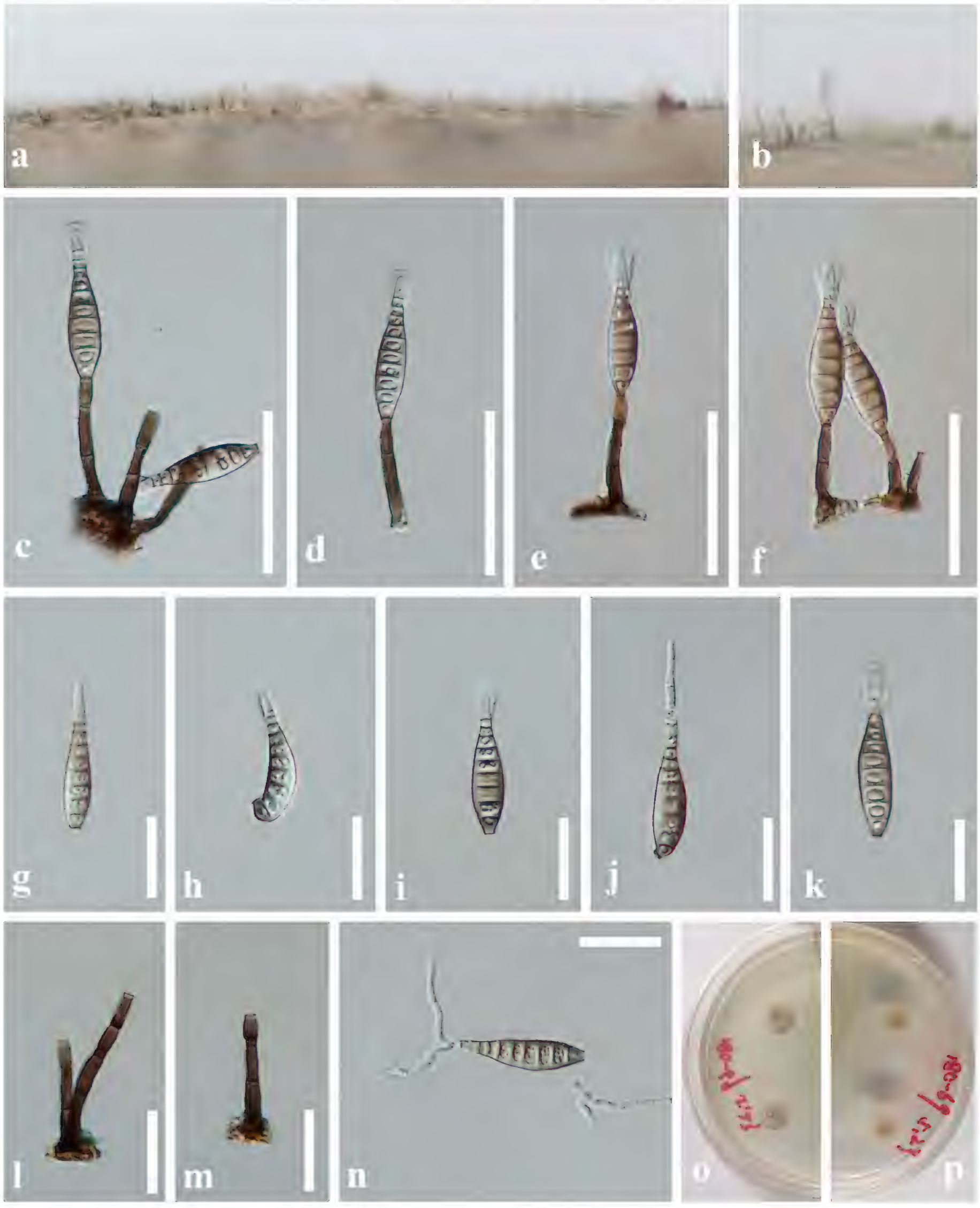

Figure 2. *Xenosporidesmium caohaiense* (HKAS 150269, holotype) **a, b.** Colony on wood; **c–f.** Conidiophores and conidia; **g–k.** Conidia; **l, m.** Conidiophores with conidiogenous cells; **n.** Germinated conidium; **o, p.** Culture; **o.** from above; **p.** from below. Scale bars: 50 µm (**c–f, l, m**); 25 µm (**g–m, n**).

cells,and conidia. Although *X. caohaiense* and *X. olivaceoconidium* exhibit highly similar morphological characteristics, they are phylogenetically distant in the tree. Additionally, there are 43 bp differences (313 bp, without gaps) in the ITS region between these two species. Therefore, we introduce *Xenosporidesmium caohaiense* as a novel species here.

Table 2. Comparative morphological characteristics of *Xenosporidesmium* species.

Taxa	Strain	Conidiophores	Conidiogenous cells	Conidia
X. aquaticivaginatum	MFLUCC 15-0624	60–125 × 4–6	NA	49.5–80.5 × 10.5–14,6–10-distoseptate, with a sheath
X. caohaiense	GZCC 19-0534	25.5–50 × 3.5–6	(6–)9–14.5 × 2.5–5.5	35–51 × 7.5–11, 8–13-distoseptate, with a sheath
X. filiforme	HKAS 130435	22–54 × 3.5–4.9 µm	12–16 × 3.6–4.9 µm	53–100 × 5.8–9.5 µm, mostly 10-distoseptate, with an apical appendage
X. guizhouense	CGMCC3.19605	23–59 × 2–4.6	13–25 × 3.1–4	46–86 × 7–11.4, 6– 10-septate, with a sheath
X. guttulatum	KUNCC 23-13374	26–55 × 3.4–5 µm	12– 20 × 3–4.8 µm	44–84 × 8.7–12 µm,6–14-distoseptate, with a sheath
X. nujiangense	DLUCC 983	31–51 × 4–5.5 µm	11.5–16.5 × 4–5 µm	54–69 × 10–12.5 µm, 10–14-septate, with a sheath
X. olivaceoconidium	MFLUCC 15-0380	25–55 × 3–4	11– 15 × 3–5	25–50 × 6–10, 9–16-septate, with a sheath

New combinations

Xenosporidesmium aquaticivaginatum **(Jing Yang & K.D. Hyde) L. L. Liu & Z. Y. Liu, comb. nov.**
Index Fungorum: IF904253

≡ *Sporidesmium aquaticivaginatum* Jing Yang & K.D. Hyde, Fungal Diversity 80: 217 (2016)

Material examined. Thailand • Prachuap Khiri Khan Province, Hua Hin, stream flowing outside Kaeng Krachan National Park, on submerged wood, 25 December 2014, Jaap van Strien, Site4-44-2 (MFLU 15-1159, holotype); ex-type living culture, MFLUCC15-0624; ibid. (HKAS950 46, isotype).

Xenosporidesmium filiforme **(W.P. Wang, H.W. Shen, K.D. Hyde & Z.L. Luo) L. L. Liu & Z. Y. Liu, comb. nov.**
Index Fungorum: IF904254

≡ *Sporidesmium filiforme* W.P. Wang, H.W. Shen, K.D. Hyde & Z.L. Luo, Mycosphere15(1): 6617 (2024)

Material examined. China • Yunnan Province, Wenshan Zhuang and Miao Autonomous Prefecture, Bamei Town, on submerged decaying wood, 7 February 2022, W.P. Wang, S-3826 (HKAS 130435, holotype).

Xenosporidesmium guizhouense **(L. L. Liu & Z. Y. Liu) L. L. Liu & Z. Y. Liu, comb. nov.**
Index Fungorum: IF904255

≡ *Sporidesmium guizhouense* L.L. Liu & Z.Y. Liu, Phytotaxa 422(2): 149 (2019)

Material examined. China • Guizhou Province, Guiyang City, Baihua Lake, 26°39.29'N, 106°32.22'E, on submerged decaying twig, 18 April 2018, Lingling

Liu, 18B–40 (HKAS 104644 holotype, GZAAS 19–005 isotype), ex-type living cultures CGMCC 3.19605, GZCC 19–005.

Xenosporidesmium guttulatum **(W.P. Wang, H.W. Shen, K.D. Hyde & Z.L. Luo) L. L. Liu & Z. Y. Liu, comb. nov.**
Index Fungorum: IF904256

≡ *Sporidesmium guttulatum* W.P. Wang, H.W. Shen, K.D. Hyde & Z.L. Luo, Mycosphere 15(1): 6617 (2024)

Material examined. China • Yunnan Province, Wenshan Zhuang and Miao Autonomous Prefecture, Bamei Town, on submerged decaying wood, 7 February 2022, W.P. Wang, S-3481 (HKAS 131397, holotype), ex-type living cultures CGMCC 3.27021 = KUNCC 23–13374.

Xenosporidesmium nujiangense **(D.F. Bao, Hong Y. Su, K.D. Hyde & Z.L. Luo) L. L. Liu & Z. Y. Liu, comb. nov.**
Index Fungorum: IF904257

≡ *Sporidesmium nujiangense* D.F. Bao, Hong Y. Su, K.D. Hyde & Z.L. Luo, J. Fungi 7(no. 669): 15 (2021)

Material examined. China • Yunnan Province, Nujiang River, on submerged decaying wood, in July 2016, Z.L. Luo, S983 (HKAS 115795, holotype), ex-type living culture, DLUCC 983.

Xenosporidesmium olivaceoconidium **(J. Yang & K.D. Hyde) L. L. Liu & Z. Y. Liucomb. nov.**
Index Fungorum: IF904258

≡ *Sporidesmium olivaceoconidium* Jing Yang & K.D. Hyde, Fungal Diversity 80: 220 (2016)

Material examined. Thailand • Chiang Rai Province, stream flowing in Tham Luang Nang Non Cave, on submerged wood, 25 November 2014, Jing Yang YJ-14 (MFLU 15-1175, holotype), ex-type living culture, MFLUCC 15-0380, GZCC 16-0008.

Discussion

Fresh samples and sequence data are urgently needed to resolve other sporidesmium-like and polyphyletic genera. For example, *Linkosia* was phylogenetically placed in three subclasses (Diaporthomycetidae, Hypocreomycetidae, Sordariomycetidae) in Sordariomycetes (Yang et al. 2018). However, its type species, *Linkosia coccothrinacis* is rarely studied and lacks molecular data, resulting in the natural classification of *Linkosia* unsettled. *Ellisembia* is another sporidesmium-like genus that differs from *Sporidesmium* in having distoseptate

conidia (Subramanian 1992). *Ellisembia* was synonymized with *Sporidesmium* by Su et al. (2016), but the same with *Linkosia*, the systematic placement of the type species of *Ellisembia*, *E. coronate* is unknown. Thus, the phylogenetic affinities between *Ellisembia* and *Sporidesmium* need to be further revealed. Due to the largely morphological similarity of *sporidesmium*-like species, we strongly recommend the inclusion of molecular evidence when introducing new taxa into this group to prevent taxonomic confusion in the future.

The Sporidesmiaceae was originally established by Fries (1849), and forms a monophyletic group, currently represented by 20 phylogenetic species (Wang et al. 2024). However, neither the original generic type *Sporidesmium atrum* nor the lectotype *S. ehrenbergii* was included in phylogenetic analyses due to the lack of sequence data. Notably, several sporidesmium-like families exist, such as Distoseptisporaceae (Su et al. 2016; Yang et al. 2021; Zhang et al. 2022; Shen et al. 2024;), Neomassariaceae (Zhang et al. 2024; Xiao et al. 2025; Sun et al. 2025), Pseudosporidesmiaceae (Crous 2008; Crous et al. 2017), and Xenosporidesmiaceae (this study). The family affiliations of *Sporidesmium atrum* and *S. ehrenbergii* need to be further revealed.

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Additional information

Conflict of interest

The authors have declared that no competing interests exist.

Ethical statement

No ethical statement was reported.

Use of AI

No use of AI was reported.

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Author contributions

Conceptualization, writing—original draft, data curation, and methodology: Ling-Ling Liu; Investigation and sample collection: Xiao-Feng Gu; Writing—review and editing: Yong-Xiang Liu; Software: Ya-Ya Chen; Formal analysis: Zuo-Yi Liu; Funding acquisition: Jia-Hai Wu; Project administration: Jiu-Lan Gou; All the authors have read and agreed to the published version of the manuscript.

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Data availability

All of the data that support the findings of this study are available in the main text.

References

Capella-Gutierrez S, Silla-Martinez JM, Gabaldon T (2009) trimAl: A tool for automated alignment trimming in large-scale phylogenetic analyses. Bioinformatics (Oxford, England) 25: 1972–1973. https://doi.org/10.1093/bioinformatics/btp348

Crous PW (2008) *Sporidesmium knawiae* Crous, sp. nov. Fungal Planet: 29.

Crous PW, Wingfield MJ, Burgess TI, Carnegie AJ, Hardy GESJ, Smith D, Summerell BA, Cano-Lira JF, Guarro J, Houbraken J, Lombard L, Martín MP, Sandoval-Denis M, Alexandrova AV, Barnes CW, Baseia IG, Bezerra JDP, Guarnaccia V, May TW, Hernández-Restrepo M, Stchigel AM, Miller AN, Ordoñez ME, Abreu VP, Accioly T, Agnello C, Agustin Colmán A, Albuquerque CC, Alfredo DS, Alvarado P, Araújo-Magalhães GR, Arauzo S, Atkinson T, Barili A, Barreto RW, Bezerra JL, Cabral TS, Camello Rodríguez F, Cruz RHSF, Daniëls PP, da Silva BDB, de Almeida DAC, de Carvalho Júnior AA, Decock CA, Delgat L, Denman S, Dimitrov RA, Edwards J, Fedosova AG, Ferreira RJ, Firmino AL, Flores JA, García D, Gené J, Giraldo A, Góis JS, Gomes AAM, Gonçalves CM, Gouliamova DE, Groenewald M, Guéorguiev BV, Guevara-Suarez M, Gusmão LFP, Hosaka K, Hubka V, Huhndorf SM, Jadan M, Jurjević Ž, Kraak B, Kučera V, Kumar TKA, Kušan I, Lacerda SR, Lamlertthon S, Lisboa WS, Loizides M, Luangsa-Ard JJ, Lysková P, Mac Cormack WP, Macedo DM, Machado AR, Malysheva EF, Marinho P, Matočec N, Meijer M, Mešić A, Mongkolsamrit S, Moreira KA, Morozova OV, Nair KU, Nakamura N, Noisripoom W, Olariaga I, Oliveira RJV, Paiva LM, Pawar P, Pereira OL, Peterson SW, Prieto M, Rodríguez-Andrade E, Rojo De Blas C, Roy M, Santos ES, Sharma R, Silva GA, Souza-Motta CM, Takeuchi-Kaneko Y, Tanaka C, Thakur A, Smith MT, Tkalčec Z, Valenzuela-Lopez N, Van der Kleij P, Verbeken A, Viana MG, Wang XW, Groenewald JZ (2017) Fungal Planet description sheets: 625–715. Persoonia 39: 270–467. https://doi.org/10.3767/persoonia.2017.39.11

Crous PW, Wingfield MJ, Burgess TI, Hardy GESJ, Gené J, Guarro J, Baseia IG, García D, Gusmão LFP, Souza-Motta CM, Thangavel R, Adamčík S, Barili A, Barnes CW, Bezerra JDP, Bordallo JJ, Cano-Lira JF, de Oliveira RJV, Ercole E, Hubka V, Iturrieta-González I, Kubátová A, Martín MP, Moreau PA, Morte A, Ordoñez ME, Rodríguez A, Stchigel AM, Vizzini A, Abdollahzadeh J, Abreu VP, Adamčíková K, Albuquerque GMR, Alexandrova AV, Álvarez Duarte E, Armstrong-Cho C, Banniza S, Barbosa RN, Bellanger JM, Bezerra JL, Cabral TS, Caboň M, Caicedo E, Cantillo T, Carnegie AJ, Carmo LT, Castañeda-Ruiz RF, Clement CR, Čmoková A, Conceição LB, Cruz RHSF, Damm U, da Silva BDB, da Silva GA, da Silva RMF, de A Santiago ALCM, de Oliveira LF, de Souza CAF, Déniel F, Dima B, Dong G, Edwards J, Félix CR, Fournier J, Gibertoni TB, Hosaka K, Iturriaga T, Jadan M, Jany JL, Jurjević Ž, Kolařík M, Kušan I, Landell MF, Leite Cordeiro TR, Lima DX, Loizides M, Luo S, Machado AR, Madrid H, Magalhães OMC, Marinho P, Matočec N, Mešić A, Miller AN, Morozova OV, Neves RP, Nonaka K, Nováková A, Oberlies NH, Oliveira-Filho

JRC, Oliveira TGL, Papp V, Pereira OL, Perrone G, Peterson SW, Pham THG, Raja HA, Raudabaugh DB, Řehulka J, Rodríguez-Andrade E, Saba M, Schauflerová A, Shivas RG, Simonini G, Siqueira JPZ, Sousa JO, Stajsic V, Svetasheva T, Tan YP, Tkalčec Z, Ullah S, Valente P, Valenzuela-Lopez N, Abrinbana M, Viana Marques DA, Wong PTW, Xavier de Lima V, Groenewald JZ (2018) Fungal Planet description sheets: 716–784. Persoonia 40: 240–393. https://doi.org/10.3767/persoonia.2018.40.10

Dong W, Hyde KD, Jeewon R, Doilom M, Yu XD, Wang GN, Liu NG, Hu DM, Nalumpang S, Zhang H (2021) Towards a natural classification of annulatascaceae-like taxa II: Introducing five new genera and eighteen new species from freshwater. Mycosphere 12: 1–88. https://doi.org/10.5943/mycosphere/12/1/1

Ellis MB (1958) *Clasterosporium* and some allied dematiaceae-phragmosporae. I. Mycological Papers 70: 1–89.

Ellis MB (1971) Dematiaceous hyphomycetes. Commonwealth Mycological Institute, Kew, Surrey, England, 594 pp. https://doi.org/10.1079/9780851986180.0000

Fries EM (1849) Summa vegetabilium Scandinaviae II. Sectio posterior, Upsaliae.

Hernández-Gutiérrez A, Sutton BC (1997) *Imimyces* and *Linkosia*, two new genera segregated from *Sporidesmium* sensu lato, and redescription of *Polydesmus*. Mycological Research 101: 201–209. https://doi.org/10.1017/S0953756296002419

Hyde KD, Hongsanan S, Jeewon R, Bhat DJ, McKenzie EHC, Jones EBG, Phookamsak R, Ariyawansa HA, Boonmee S, Zhao Q, Abdel-Aziz FA, Abdel-Wahab MA, Banmai S, Chomnunti P, Cui BK, Daranagama DA, Das K, Dayarathne MC, de Silva NI, Dissanayake AJ, Doilom M, Ekanayaka AH, Gibertoni TB, Go'esNeto A, Huang SK, Jayasiri SC, Jayawardena RS, Konta S, Lee HB, Li WJ, Lin CG, Liu JK, Lu YZ, Luo ZL, Manawasinghe IS, Manimohan P, Mapook A, Niskanen T, Norphanphoun C, Papizadeh M, Perera RH, Phukhamsakda C, Richter C, de Santiago ALCMA, Drechsler-Santos ER, Senanayake IC, Tanaka K, TMDS T, Thambugala KM, Tian Q, Tibpromma S, Thongbai B, Vizzini A, Wanasinghe DN, Wijayawardene NN, Wu HX, Yang J, Zeng XY, Zhang H, Zhang JF, Bulgakov TS, Camporesi E, Bahkali AH, Amoozegar MA, Araujo-Neta LS, Ammirati JF, Baghela A, Bhatt RP, Bojantchev D, Buyck B, da Silva GA, de Lima CLF, de Oliveira RJV, de Souza CAF, Dai YC, Dima B, Duong TT, Ercole E, MafaldaFreire F, Ghosh F, Hashimoto A, Kamolhan S, Kang JC, Karunarathna SC, Kirk PM, Kytövuori I, Lantieri A, Liimatainen K, Liu ZY, Liu XZ, Lücking R, Medardi G, Mortimer PE, TTT N, Promputtha I, KNA R, Reck MA, Lumyong S, Shahzadeh-Fazeli SA, Stadler M, Soudi MR, Su HY, Takahashi T, Tangthirasunun N, Uniyal P, Wang Y, Wen TC, Xu JC, Zhang ZK, Zhao YC, Zhou JL, Zhu L (2016) Fungal diversity notes 367–490: taxonomic and phylogenetic contributions to fungal taxa. Fungal diversity 80: 1–270. https://doi.org/10.1007/s13225-016-0373-x

Hyde KD, Norphanphoun C, Maharachchikumbura SSN, Bhat DJ, Jones EBG, Bundhun D, Chen YJ, Bao DF, Boonmee S, Calabon MS, Chaiwan N, Chethana KWT, Dai DQ, Dayarathne MC, Devadatha B, Dissanayake AJ, Dissanayake LS, Doilom M, Dong W, Fan XL, Goonasekara ID, Hongsanan S, Huang SK, Jayawardena RS, Jeewon R, Karunarathna A, Konta S, Kumar V, Lin CG, Liu JK, Liu NG, Luangsa-ard J, Lumyong S, Luo ZL, Marasinghe DS, McKenzie EHC, Niego AGT, Niranjan M, Perera RH, Phukhamsakda C, Rathnayaka AR, Samarakoon MC, Samarakoon SMBC, Sarma VV, Senanayake IC, Shang QJ, Stadler M, Tibpromma S, Wanasinghe DN, Wei DP, Wijayawardene N, Xiao YP, Yang J, Zeng XY, Zhang SN, Xiang MM (2020) Refined families of Sordariomycetes. Mycosphere 11: 305–1059. https://doi.org/10.5943/mycosphere/11/1/7

Index Fungorum (2025) Index Fungorum. http://www.indexfungorum.org/names/names.asp

Katoh K, Standley DM (2013) MAFFT multiple sequence alignment software version 7: Improvements in performance and usability. Molecular Biology and Evolution 30: 772–780. https://doi.org/10.1093/molbev/mst010

Link HF (1809) Observationes in ordines plantarum naturales. Dissertatio I. Magazin der Gesellschaft Naturforschenden Freunde Berlin 3: 3–42.

Liu YJ, Whelen S, Hall BD (1999) Phylogenetic relationships among ascomycetes: Evidence from an RNA polymerse II subunit. Molecular Biology and Evolution 16: 1799–1808. https://doi.org/10.1093/oxfordjournals.molbev.a026092

Liu LL, Yang J, Liu NG, Chen YY, Gui XX, Liu ZY (2019) *Sporidesmium guizhouense* sp. nov. (Sordariomycetes *incertae sedis*), a new species from a freshwater habitat in Guizhou Province, China. Phytotaxa 422: 144–156. https://doi.org/10.11646/phytotaxa.422.2.2

Luo ZL, Hyde KD, Liu JK, Maharachchikumbura SSN, Jeewon R, Bao DF, Bhat DJ, Lin CG, Li WL, Yang J, Liu NG, Lu YZ, Jayawardena RS, Li JF, Su HY (2019) Freshwater Sordariomycetes. Fungal Diversity 99: 451–660. https://doi.org/10.1007/s13225-019-00438-1

McKenzie EHC (1995) Dematiaceous Hyphomycetes on Pandanaceae. 5. *Sporidesmium sensu lato*. Mycotaxon 56: 9–29.

Nguyen T, Schmidt HA, von Haeseler A, Minh BQ (2014) IQ-TREE: A fast and effective stochastic algorithm for estimating maximum-likelihood phylogenies. Molecular Biology and Evolution 32: 268–274. https://doi.org/10.1093/molbev/msu300

Nylander JAA (2008) MrModeltest 2.3. Uppsala, Department of Systematic Zoology, Uppsala University.

Rathnayaka AR, Tennakoon DS, Jones EBG, Wanasinghe DN, Bhat DJ, Priyashantha AH, Stephenson SL, Tibpromma S, Karunarathna SC (2025) Significance of precise documentation of hosts and geospatial data of fungal collections, with an emphasis on plant-associated fungi. New Zealand Journal of Botany 63(2–3): 462–489. https://doi.org/10.1080/0028825X.2024.2381734

Réblová M (1999) Studies in *Chaetosphaeria sensu lato* III. *Umbrinosphaeria* gen. nov. and *Miyoshiella* with *Sporidesmium* anamorphs. Mycotaxon 71: 13–43.

Ronquist F, Teslenko M, Van Der Mark P, Ayres DL, Darling A, Höhna S, Larget B, Liu L, Suchard MA, Huelsenbeck JP (2012) MrBayes 3.2: Efficient Bayesian phylogenetic inference and model choice across a large model space. Systematic Biology 61: 539–542. https://doi.org/10.1093/sysbio/sys029

Senanayake I, Rathnayaka AR, Marasinghe DS, Calabon MS, Gentekaki E, Lee HB, Hurdeal VG, Pem D, Dissanayake LS, Wijesinghe SN, Bundhun D, Nguyen TT, Goonasekara ID, Abeywickrama PD, Bhunjun CS, Jayawardena RS, Wanasinghe DN, Jeewon R, Bhat DJ, Xiang MM (2020) Morphological approaches in studying fungi: Collection, examination, isolation, sporulation and preservation. Mycosphere 11: 2678–2754. https://doi.org/10.5943/mycosphere/11/1/20

Shen HW, Bao DF, Boonmee S, Lu YZ, Su XJ, Li YX, Luo ZL (2024) Diversity of *Distoseptispora* (Distoseptisporaceae) taxa on submerged decaying wood from the Red River in Yunnan, China. MycoKeys 102: 1–28. https://doi.org/10.3897/mycokeys.102.116096

Shenoy BD, Jeewon R, Wu WP, Bhat DJ, Hyde KD (2006) Ribosomal and RPB2 DNA sequence analyses suggest that *Sporidesmium* and morphologically similar genera are polyphyletic. Mycological Research 110: 916–928. https://doi.org/10.1016/j.mycres.2006.06.004

Shoemaker RA, Hambleton S (2001) *"Helminthosporium" asterinum*, *Polydesmus elegans*, *Imimyces*, and allies. Canadian Journal of Botany 79: 592–599. https://doi.org/10.1139/b01-038

Su HY, Hyde KD, Maharachchikumbura SSN, Ariyawansa HA, Luo ZL, Promputtha I, Tian Q, Lin CG, Shang QJ, Zhao YC (2016) The families Distoseptisporaceae fam. nov., Kirschsteiniotheliaceae, Sporormiaceae and Torulaceae, with new species from freshwater in Yunnan Province, China. Fungal Diversity 80: 375–409. https://doi.org/10.1007/s13225-016-0362-0

Subramanian CV (1992) A reassessment of *Sporidesmium* (Hyphomycetes) and some related taxa. Proceedings of the Indian National Science Academy Part B 58: 179–179.

Sun YR, Hyde KD, Liu NG, Jayawardena RS, Wijayawardene NN, Ma J, Zhang Q, Al-Otibi F, Wang Y (2025) Micro-fungi in southern China and northern Thailand: Emphasis on medicinal plants. Fungal Diversity 131: 99–299. https://doi.org/10.1007/s13225-024-00549-4

Vaidya G, Lohman DJ, Meier R (2011) SequenceMatrix: Concatenation software for the fast assembly of multi-gene datasets with character set and codon information. Cladistics : The International Journal of the Willi Hennig Society 27: 171–180. https://doi.org/10.1111/j.1096-0031.2010.00329.x

Vilgalys R, Hester M (1990) Rapid genetic identification and mapping of enzymatically amplified ribosomal DNA from several *Cryptococcus* species. Journal of Bacteriology 172: 4238–4246. https://doi.org/10.1128/jb.172.8.4238-4246.1990

Wang F, Wang K, Cai L, Zhao MJ, Kirk PM, Fan GM, Sun QL, Li B, Wang S, Yu ZF (2022) Fungal names: A comprehensive nomenclatural repository and knowledge base for fungal taxonomy. Nucleic Acids Research 51: D708–D716. https://doi.org/10.1093/nar/gkac926

Wang WP, Hyde KD, Bao DF, Wanasinghe DN, Lin CG, Shen HW, Lu YZ, Zhang ZQ, Su XJ, Li YX, Al-Otibi F, Yang LQ, Luo ZL (2024) Lignicolous freshwater fungi from karst landscapes in Yunnan Province, China. Mycosphere 15: 6525–6640. https://doi.org/10.5943/mycosphere/15/1/29

White TJ, Bruns T, Lee S, Taylor J (1990) Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. In: Innis MA, Gelfand DH, Sninsky JJ, White TJ (Eds) PCR protocols: a guide to methods and applications. Academic Press, San Diego, 315–322. https://doi.org/10.1016/B978-0-12-372180-8.50042-1

Wu WP, Zhuang WY (2005) *Sporidesmium*, *Endophragmiella* and related genera from China. Fungal Diversity Research Series 15: 1–351.

Xiao XJ, Liu NG, Liu JK, Shen HW, Yu YX, Yu XD, Xiao Y, Tian XG, Han MY, Bao DF, Liu JW, Yang Y, Ma J, Zhang JY, Sun YR, Luo ZL, Hongsanan S, Xiao YP, Jayawardena RS, Lu YZ, Sun JZ (2025) Fungal Diversity of Ascomycota in China and Thailand: Descriptions of New Taxa in Honour of Kevin D. Hyde's 70th Birthday. Mycosphere (in press).

Yang J, Maharachchikumbura SSN, Liu JK, Hyde KD, Jones EBG, Al-Sadi AM, Liu ZY (2018) *Pseudostanjehughesia aquitropica* gen. et sp. nov. and *Sporidesmium* sensu lato species from freshwater habitats. Mycological Progress 17: 591–616. https://doi.org/10.1007/s11557-017-1339-4

Yang J, Liu LL, Jones EBG, Li WL, Hyde KD, Liu ZY (2021) Morphological variety in *Distoseptispora* and introduction of six novel species. Journal of Fungi (Basel, Switzerland) 7: 945. https://doi.org/10.3390/jof7110945

Zhang H, Zhu R, Qing Y, Yang H, Li CX, Wang GN, Zhang D, Ning P (2022) Polyphasic identification of *Distoseptispora* with six new species from fresh water. Journal of Fungi (Basel, Switzerland) 8: 1063. https://doi.org/10.3390/jof8101063

Zhang SN, Hyde KD, Jones EBG, Yu XD, Cheewangkoon R, Liu JK (2024) Current insights into palm fungi with emphasis on taxonomy and phylogeny. Fungal Diversity 127: 55–301. https://doi.org/10.1007/s13225-024-00536-9